Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1-41. (Cancelled)

42. (Currently Amended) A method for performing genotypic classification of fluorescence data generated by ~~polymorphic~~ analysis of a DNA sample, comprising:

(a) receiving a data set generated by a fluorometric genotyping device, the data set comprising fluorescence dye emissions for one or more pairs of probes, the probes of the probe pairs comprising different dyes and being specific for different alleles, wherein the relative intensity of fluorescence dye emissions is reflective of the allelic composition of the DNA sample;

(b) plotting the fluorescence dye emissions of the data set on a graph with a first axis representing a first dye emission associated with a first allele and a second axis representing a second dye emission associated with a second allele;

(c) generating angular values for each of the probe pairs of the data set based on the relative intensity of fluorescence dye emissions with respect to one another as plotted on the graph;

(d) sorting the set of angle values generated in step (c) to produce an ordered set of angular values;

~~(d)~~ (e) generating a set of angular difference values by subtracting ~~one~~ a previous angular value from a ~~next~~ current angular value of the ordered set of angular values, for each adjacent pair of the ordered set of angular values;

~~(e)~~ (f) ~~identifying at least one category-dividing angular value by identifying at least one of the ordered set of angular values for which~~ determining if the angular difference value of at least one of the ordered set of angular values differs from the previous angular difference value ~~differs~~ by at least a predetermined difference threshold;

(g) if the angular difference value of at least one of the ordered set of angular values is determined to differ from one previous angular value by at least the predetermined difference threshold, determining at least one category-dividing angular value based on the at least one of the ordered set of angular values;

~~(f)~~ (h) classifying the genotype of the DNA sample based on the plotted fluorescence dye emissions of each probe pair ~~and their locality~~ with respect to the at least one category-dividing angular value to generate classification results when the at least one category-dividing angular value is identified; and

~~(g)~~ (i) outputting ~~the classified genotype of the DNA sample~~ generated classification results.

43. (Previously Presented) The method of claim 42, wherein the at least one category-

dividing angular value divides the data set into at least two categories selected from homozygous for the first allele, homozygous for the second allele, heterozygous, and an absence of the first allele and second allele.

44. (Previously Presented) The method of claim 43, wherein the at least one category-dividing angular value divides the data set into the categories of homozygous for the first allele, homozygous for the second allele, heterozygous, and an absence of the first allele and second allele, each category being represented by a quadrant of the graph.

45. (Previously Presented) The method of claim 42, wherein the generating angular values of step (c) comprises computing an arctangent of the first and second dye emissions.

46-47. (Cancelled)

48. (Currently Amended) The method of claim ~~46, wherein the at least one predetermined condition is based on~~ 42, further comprising calculating a range between a maximum and minimum fluorescence dye emission for at least one probe of the probe pairs.

49. (New) The method of claim 48, further comprising determining the at least one probe to be invalid if the range falls below a first predetermined threshold.

50. (New) The method of claim 48, wherein calculating a range comprises calculating a range between a maximum and minimum fluorescence dye emission for each probe of the probe pairs.

51. (New) The method of claim 50, further comprising normalizing the data set if the range for each probe exceeds a second predetermined threshold.

52. (New) The method of claim 51, further comprising computing a Euclidean distance between a minimum value of the data set and each of the probe pairs.

53. (New) The method of claim 52, further comprising removing probe pairs from the data set whose Euclidean distance falls below a predetermined distance threshold.

54. (New) The method of claim 53, further comprising computing an average Euclidean distance of probe pairs remaining in the data set after the removing.

55. (New) The method of claim 54, further comprising calculating an average distance threshold based on the average Euclidean distance, and removing pairs of the remaining probe pairs that fall below the average distance threshold.

56. (New) The method of claim 42, further comprising evaluating the classification results to

determine whether to flag the classification results for review based on predetermined conditions.

57. (New) The method of claim 56, wherein the predetermined conditions comprise at least one of: excess classification in one category, classification into more than three categories, absence or near absence of classification in at least one category, the presence of unclassified probe pairs in the data set inadequate separation of probe pairs from control or nonamplification reactions, categorization of probe pairs into a least one category whose category-dividing angular value is greater than an angular maximum or less than an angular minimum, categorization of probe pairs into a category whose angular width is greater than an angular width threshold, the presence of classification results that are incompatible with a Hardy-Weinberg Equilibrium, the presence of control or nonamplification reactions whose distance from the origin exceeds a control distance threshold, classification of all probe pairs into a homozygous category, classification into only one category that is not determined to be all homozygous, and classification into a heterozygous category of a number of probe pairs that is greater than a heterozygous threshold.

58. (New) A method for performing genotypic classification of fluorescence data generated by analysis of a DNA sample, comprising:

(a) receiving a data set generated by a fluorometric genotyping device, the data set comprising fluorescence dye emissions for one or more pairs of probes, the probes of the probe pairs comprising different dyes and being specific for different alleles, wherein the relative intensity of fluorescence dye emissions is reflective of the allelic composition of the DNA

sample;

(b) plotting the fluorescence dye emissions of the data set on a graph with a first axis representing a first dye emission associated with a first allele and a second axis representing a second dye emission associated with a second allele;

(c) generating angular values for each of the probe pairs of the data set based on the relative intensity of fluorescence dye emissions with respect to one another as plotted on the graph;

(d) sorting the set of angle values generated in step (c) to produce an ordered set of angular values;

(e) generating a set of angular difference values by subtracting a previous angular value from a current angular value of the ordered set of angular values, for each adjacent pair of the ordered set of angular values;

(f) determining that the angular difference value of at least one of the ordered set of angular values differs from the previous angular difference value by at least a predetermined difference threshold;

(g) determining at least one category-dividing angular value based on the at least one ordered set of angular values, for the at least one of the ordered set of angular values that is determined in step (f) to have an angular difference value that differs from one previous angular value by at least the predetermined difference threshold;

(h) classifying the genotype of the DNA sample based on the plotted fluorescence dye emissions of each probe pair with respect to the at least one category-dividing angular value to

generate classification results when the at least one category-dividing angular value is identified;

and

(i) outputting generated classification results.